

1

SEQUENCE LISTING

<110> Presnell, Scott R.  
Kuestner, Rolf E.  
Gao, Zeren

<120> HUMAN CYTOKINE RECEPTOR

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Met Ala Pro Trp Leu Gln Leu Cys Ser  
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gtc ttc ttt acg gtc aac gcc tgc ctc aac ggc tcg cag ctg gct gtg 160  
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Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp Thr Cys Gly Trp  
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Arg Met Lys Ala Ala Arg Pro Arg Leu Cys Val Ala Asn Glu Gly  
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gtg ggg cca gcc agc aga aac agt ggg ctg tac aac atc acc ttc aaa 304  
Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys  
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Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile  
75 80 85

gct gac gcc cag aat atc acc atc agc cag tat gct tgc cat gac caa 400  
Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln  
90 95 100 105

gtg gca gtc acc att ctt tgg tcc cca ggg gcc ctc ggc atc gaa ttc 448  
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	110	115	120	
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cag tgc caa caa ctg att cta aag gat ccg aag cag ctc aac agt agc Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser	140	145	150	544
ttc aaa aga act gga atg gaa tct caa cct ttc ctg aat atg aaa ttt Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe	155	160	165	592
gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att aaa aac Glu Thr Asp Tyr Phe Val Lys Val Pro Phe Pro Ser Ile Lys Asn	170	175	180	640
gaa agc aat tac cac cct ttc ttc ttt aga acc cga gcc tgt gac ctg Glu Ser Asn Tyr His Pro Phe Phe Arg Thr Arg Ala Cys Asp Leu	190	195	200	688
ttg tta cag ccg gac aat cta gct tgt aaa ccc ttc tgg aag cct cgg Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg	205	210	215	736
aac ctg aac atc agc cag cat ggc tcg gac atg cag gtg tcc ttc gac Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser Phe Asp	220	225	230	784
cat gca ccg cac aac ttc ggc ttc cgt ttc tat ctt cac tac aag His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys	235	240	245	832
ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag gag caa Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln	250	255	260	880
act aca gag acg acc agc tgc ctc ctt caa aat gtt tct cca ggg gat Thr Thr Glu Thr Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp	270	275	280	928
tat ata att gag ctg gtg gat gac act aac aca aca aga aaa gtg atg Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Arg Lys Val Met	285	290	295	976
cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc atc aga His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg	300	305	310	1024
gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc gcg acg Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr	315	320	325	1072
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gcc ctt gac ggt agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa Ala Leu Asp Gly Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys 650	655	660	2080
gcc ggc agc ccc tcg gac atg ccg cg <sup>g</sup> gac tca ggc atc tat gac tcg Ala Gly Ser Pro Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser 670	675	680	2128
tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser 685	690	695	2176
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Pro Arg Leu Cys Val Ala Asn Glu Gly Val Gly Pro Ala Ser Arg Asn 50 55 60			
Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr Thr Tyr 65 70 75 80			
Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn Ile Thr 85 90 95			
Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp 100 105 110			
Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile 115 120 125			

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 Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly Met Glu  
 145 150 155 160  
 Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys  
 165 170 175  
 Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe  
 180 185 190  
 Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu  
 195 200 205  
 Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His  
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 Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe Gly  
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 Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro Phe  
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 Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro Val  
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 His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro  
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 Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Ser  
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 Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg Pro  
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 Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn His  
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 Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu  
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 Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe Ile  
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 Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn  
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 Tyr Lys His Lys Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu Phe  
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 Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp Tyr  
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 Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys Tyr  
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 Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser Arg  
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Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly Gly  
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 Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp Met  
 660 665 670  
 Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu  
 675 680 685  
 Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr Ser  
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 Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys Ala  
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 ytnaayccrig tngnaarca ygtntgcn gaygencara ayathacnat hwsncartay 300  
 gcntgycayg aycargtngc ngtnacnath ytniggwsnc cnngngcnyt ngnathgar 360  
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 carytnathy tnaargaycc naarcarytn aaywsnwsnt tyaarmgnac ngnatggar 480  
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 ccnwsnatha araaygarws naaytacyc ccnattyttt tymgnacnmg ncntgygay 600  
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 tgyaarcarg arcaracnac ngaracnacn wsntgyytny tncaraaygt nwsncnngn 840  
 gaytayatha thgarytnytngt ngaygayan aayacnacnm gnaargtnat gcaytaygcn 900  
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       60           65           70

tat gac aat tgt acc acc tac ttg aat cca gtg ggg aag cat gtg att 352  
 Tyr Asp Asn Cys Thr Thr Tyr Leu Asn -Pro Val Gly Lys His Val Ile  
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110          115          120

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Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg  
125 130 135

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cag tgc caa caa ctg att cta aag gat ccg aag cag ctc aac aac agt agc 544
Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser
          140           145           150

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gaa agc aat tac cac cct ttc ttc ttt aga acc cga gcc tgt gac ctg Glu Ser Asn Tyr His Pro Phe Phe Arg Thr Arg Ala Cys Asp Leu 190 195 200	688
ttg tta cag ccg gac aat cta gct tgt aaa ccc ttc tgg aag cct cg Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg 205 210 215	736
aac ctg aac atc agc cag cat ggc tcg gac atg cag gtg tcc ttc gac Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser Phe Asp 220 225 230	784
cac gca ccg cac aac ttc ggc ttc cgt ttc tat ctt cac tac aag His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys 235 240 245	832
ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag gag caa Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln 250 255 260 265	880
act aca gag atg acc agc tgc ctc ctt caa aat gtt tct cca ggg gat Thr Thr Glu Met Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp 270 275 280	928
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gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc gcg acg Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr 315 320 325	1072
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cat tta gat gaa gag agc tct gag tct tcc aca tac act gca gca ctc His Leu Asp Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu 350 355 360	1168
cca aga gag agg ctc ccg ccg ccg aag gtc ttt ctc tgc tat tcc Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser 365 , 370 375	1216
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tac ttt gtg gac aag aac tac aaa cac aaa gga ggt ggc cga ggc Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Arg Gly 445 450 455			1456
tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu 460 465 470			1504
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gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca Glu Pro Asp Trp Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro 570 575 580 585			1840
ctg cgc tac cgg gag cca gtc ttg gag aaa ttt gat tcg ggc ttg gtt Leu Arg Tyr Arg Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val 590 595 600			1888
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aag gta gag gcg gct gtt ctt ggg gca acc gga cca gcc gac tcc cag Lys Val Glu Ala Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln 620 625 630			1984
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Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His  
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 Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe Gly  
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 Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg Pro  
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 Tyr Lys His Lys Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu Phe  
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 Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser Arg  
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 Gln Phe Val Pro Phe His Pro Pro Leu Arg Tyr Arg Glu Pro Val  
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 Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val Leu  
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 625 630 635 640  
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 645 650 655  
 Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp Met  
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 Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu  
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 690 695 700

Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu Glu  
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 Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys Ala  
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 tyytnaarg gnattyngnt nathytnar garytnaaw sngarggnmg ncartygcar 420  
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 wsncarccnt tyytnaayat gaarttygar acngaytay tytqnaargt ngtncntty 540  
 ccnwsnatha araaygarws naaytaycay ccnnttyt ytmgnacnmg ncntgygay 600  
 ytntytnytn arccngayaa ytnqcntgy aarccnttyt ggaarccnmg naayytnaay 660  
 athwsncarc ayggnsnra yatgcargtn wsnttygacy aygcncnca yaaytgygn 720  
 ttymgnattytyt tytaytnca ytayaarytn aarcaygarg gnccnttyaa rmgnaaracn 780  
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 ytnaarcncng tncaywsncc ntggcnggn ccnathmgng cngtngcnat hacngtnccn 960  
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 garaayatht aywsncayyt ngaygargar wsnwsngarw snwsnacnta yacngcngcn 1080  
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 ggnccaraayc ayatgaaaygt ngtncartgy ttygcntay tyytnacrga ytttgygggn 1200  
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Met Ala Pro Trp Leu Gln Leu Cys Ser
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Val Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Val
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Arg Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr
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Phe Lys Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His
60 65 70

gtg att gct gac gcc cag aat atc acc atc agc cag tat gct tgc cat 352
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gaa ttc ctg aaa gga ttt cgg gta ata ctg gag gag ctg aag tcg gag 448
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Gly Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn
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Ser Ser Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met
140 145 150

aaa ttt gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att 592
Lys Phe Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile
155 160 165

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Lys Asn Glu Ser Asn Tyr His Pro Phe Phe Arg Thr Arg Ala Cys
170 175 180 185

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gag caa act aca gag acg acc agc tgc ctc ctt caa aat gtt tct cca Glu Gln Thr Thr Glu Thr Ser Cys Leu Leu Gln Asn Val Ser Pro 250	255	260	880
ggg gat tat ata att gag ctg gtg gat gac act aac aca aca aga aaa Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Arg Lys 270	275	280	928
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gcg acg ctc ttc act gtg atg tgc cgc aag aag caa caa gaa aat ata Ala Thr Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile 315	320	325	1072
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685	690	695	
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act gat gaa ctc cac gcg gtc gcc cct ttg taacaaaacg aaagagtcta Thr Asp Glu Leu His Ala Val Ala Pro Leu 730	735		2322
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Gln His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn 210 215 220			
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 Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser  
     645               650               655  
 Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser  
     660               665               670  
 Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu  
     675               680               685  
 Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Gly Leu Gly Glu  
     690               695               700  
 Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys  
     705               710               715               720  
 Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val  
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 Ala Pro Leu

<210> 9  
 <211> 2217  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:8.

<221> misc\_feature

<222> (1)...(2217)

<223> n = A, T, C or G

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 tggmngggng tnggnccngc nwsnmgnaaay wsnggnytnt ayaayathac nttyaartay 180  
 gayaaytgya cnacntayyt naayccngtn ggnaarcayg tnacnacntha ygcncaraay 240  
 athacnathw sncartaygc ntgycaygay cargtngcng tnacnathytn tngwsncn 300  
 gngcnytng gnathgartt yttnaarggn ttymngntna thytngarga rytnaarwsn 360  
 garginmgnc artgycarca rytnathytn aargayccna arcarytnaa ywsnwsntt 420  
 aarmgnacng gnatgarws ncarrccnty yttnaayatga arttygarac ngaytaytt 480  
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 aarccnmgnna ayytnaayat hwsncarcar ggnwsngaya tgcargtnws nttygacy 660  
 gcncncnaya aytttyggntt ymgntt yttaytnacayt ayaarytnaa rcaygarggn 720  
 ccnttyaarm gnaaracntg yaarcargar caracnacng aracnacnws ntgyytnytn 780  
 caraaygtnw snccnngnna ytayathath garytngtng aygayaacnaa yacnacnmgn 840  
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<211> 16

<212> PRT

<213> Artificial Sequence

<220>

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<211> 2443

<212> DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101) ... (2317)

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Met Ala Pro Trp Leu  
 1 5

cag ctc tgc tcc ttc ttc act gtc aac gcc tgt ctc aac ggc tcg 163  
 Gln Leu Cys Ser Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser  
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cag ctg gca gtg gcc gcg ggc tcc ggc cgc gcg agg ggc gcg gac 211  
 Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp  
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acc tgt ggc tgg agg gga gtg ggg ccg gcc agc agg aac agc gga ctg 259  
 Thr Cys Gly Trp Arg Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu  
 40 45 50

cac aac atc acc ttc aga tac gac aac tgt acc acc tac ttg aat ccc 307  
 His Asn Ile Thr Phe Arg Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro  
 55 60 65

ggc ggc ggg aag cat gcg att gct gat gct cag aac atc acc atc agc 355  
 Gly Gly Gly Lys His Ala Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser  
 70 75 80 85

cag tac gct tgc cac gac cag gtg gca gtc acc att ctt tgg tcc cca 403  
 Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp Ser Pro  
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ggg gcc ctt ggc att gaa ttc cta aaa gga ttc cga gtc atc ctg gag 451  
 Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile Leu Glu  
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gag ctg aag tcg gag ggc aga cag tgc caa cag ctg att cta aag gac 499  
 Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp  
 120 125 130

ccc aaa cag ctc aac agc agc ttc aga agg act gga atg gaa tct cag 547  
 Pro Lys Gln Leu Asn Ser Ser Phe Arg Arg Thr Gly Met Glu Ser Gln  
 135 140 145

cct ttc ctg aat atg aaa ttt gag acg gat tac ttt gta aag att gtc 595  
 Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys Ile Val  
 150 155 160 165

cct ttc cct tcc att aaa aat gaa agc aat tac cat ccc ttc ttc ttc 643  
 Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe Phe  
 170 175 180

aga aca cgg gcc tgt gac ctg ttg tta caa cct gac aac ttg gcc tgt 691  
 Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu Ala Cys  
 185 190 195

aag cct ttc tgg aag cct cga aac ctg aat atc agc cag cat ggt tct 739  
 Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His Gly Ser

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agg act tgc agg cag gac cag aat aca gag aca acc agc tgc ctc ctc Arg Thr Cys Arg Gln Asp Gln Asn Thr Glu Thr Thr Ser Cys Leu Leu 250 255 260			883
caa aac gtt tct cca ggg gac tat atc att gag ctg gtg gat gac agc Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Ser 265 270 275			931
aac acc acc agg aaa gct gct cag tat gtg gtg aag tca gtg cag tct Asn Thr Thr Arg Lys Ala Ala Gln Tyr Val Val Lys Ser Val Gln Ser 280 285 290			979
ccc tgg gct gga ccc atc aga gct gtg gcc atc act gtg cct ctg gtt Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro Leu Val 295 300 305			1027
gtc ata tct gcg ttc gca acc ctg ttc act gtg atg tgc aga aag aag Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg Lys Lys 310 315 320 325			1075
caa caa gaa aat ata tat tca cat tta gat gaa gaa agc ccg gag tcg Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Pro Glu Ser 330 335 340			1123
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gtg gct ctg gac ttg tgg gaa gat ttc agc ctc tgc aga gag ggg cag Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu Gly Gln 390 395 400 405			1315
aga gaa tgg gcc att cag aag atc cac gag tcc cag ttc atc att gtc Arg Glu Trp Ala Ile Gln Lys Ile His Glu Ser Gln Phe Ile Ile Val 410 415 420			1363
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tct gcc gca ctg cgc aag ttc atc gcc gtc tac ttc gat tat tcc tgt Ser Ala Ala Leu Arg Lys Phe Ile Ala Val Tyr Phe Asp Tyr Ser Cys 470 475 480 485	1555
gaa ggg gat gta ccc tgc agc ctg gac ctg agc acc aag tac aag ctc Glu Gly Asp Val Pro Cys Ser Leu Asp Leu Ser Thr Lys Tyr Lys Leu 490 495 500	1603
atg gac cac ctt cct gag ctc tgt gcc cat ctg cac tca gga gag cag Met Asp His Leu Pro Glu Leu Cys Ala His Leu His Ser Gly Glu Gln 505 510 515	1651
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695

700

705

acc ctc cct tcc aag ctc ttt gcc tct ggg gtg tcc aga gaa cat ggt 2275  
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 710 715 720 725

tgc cac agc cac act gac gaa ctg caa gcg ctt gct cct ttg 2317  
 Cys His Ser His Thr Asp Glu Leu Gln Ala Leu Ala Pro Leu  
 730 735

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 50 55 60  
 Thr Tyr Leu Asn Pro Gly Gly Lys His Ala Ile Ala Asp Ala Gln  
 65 70 75 80  
 Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr  
 85 90 95  
 Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe  
 100 105 110  
 Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln  
 115 120 125  
 Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Arg Arg Thr  
 130 135 140  
 Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr  
 145 150 155 160  
 Phe Val Lys Ile Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr  
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 His Pro Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro  
 180 185 190  
 Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile  
 195 200 205  
 Ser Gln His Gly Ser Asp Met His Val Ser Phe Asp His Ala Pro Gln  
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 225 230 235 240  
 Gly Pro Phe Arg Arg Thr Cys Arg Gln Asp Gln Asn Thr Glu Thr  
 245 250 255  
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 325 330 335

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 Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp  
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 Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Cys Ser Leu Asp Leu Ser  
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 Thr Lys Tyr Lys Leu Met Asp His Leu Pro Glu Leu Cys Ala His Leu  
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 Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Ile Ser  
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 Lys Pro Gly Pro Glu Ser Asp Phe Cys Arg Lys Val Glu Ala Cys Val  
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 Leu Gly Ala Ala Gly Pro Ala Asp Ser Tyr Ser Tyr Leu Glu Ser Gln  
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 His Val Gly Leu Asp Gln Asp Thr Glu Ala Gln Pro Ser Cys Asp Ser  
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 Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Gly Leu Gly  
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 Glu Glu Asp Pro Pro Thr Leu Pro Ser Lys Leu Phe Ala Ser Gly Val  
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<221> misc\_feature  
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<223> n = A, T, C or G

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wsnwsnacnt	aygcngcngc	nytncnmgn	gaymgnytnm	gnccncarcc	naargtntty	1080
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gcncncngny	tncarccnyt	nytncaygcn	gtnaargcng	gnwsncnws	ngaratgccn	1980
mngaywsng	gnathtayga	ywsnwsngtn	ccnwsnwsng	arytnwsnyt	nccnytnatg	2040
garggnytnw	snccngayca	rathgaracn	wsnwsnytna	cngarwsngt	nwsnwsnwsn	2100
wsnggnytng	gngargarga	yccnccnacn	ytnccnwsna	arytnttygc	nwsnggngtn	2160
wsnmngngarc	ayggntgyca	ywsncayacn	gaygarytnc	argcnytngc	nccnytn	2217